CYTOCHROME P450 GENETIC VARIATIONS

CROSS-REFERENCE TO RELATED APPLICATION

The present is a continuation of PCT Patent Application PCT/US03/21468 filed July 9, 2003 and a continuation-in-part of United States Patent Application 10/360,790, which claims the benefit of United States Provisional Patent Application 60/306,675 filed July 20, 2001, the contents of which are incorporated herein by reference in their entirety.

BACKGROUND

Adverse reactions to pharmaceutical drugs cause significant morbidity and mortality. Further, when the rate or severity of the adverse reactions causes the withdrawal of a pharmaceutical drug from the market, adverse reactions also cause considerable financial losses to pharmaceutical companies.

A large portion of endobiotics and xenobiotics, including many classes of pharmaceutical drugs, is metabolized by cytochrome p450 super family of enzymes present in human liver tissue. Cytochrome P450 2D6 (CYP2D6) is an isoenzyme of the cytochrome p450 super family and is responsible for the metabolism of many pharmaceutical drugs in commonly prescribed drug classes such as antiarrhythmics, ß-receptor blockers, neuroleptics, selective serotonin reuptake inhibitors and antidepressants. Examples of pharmaceutical drugs metabolized by CYP2D6 include amitriptyline, codeine, desipramine, haloperidol, metopropol, tamoxifen and timolol.

There is considerable genetic polymorphism in CYP2D6. Polymorphic variants of CYP2D6 can result in altered metabolism of pharmaceutical drugs due to impaired CYP2D6 function. The altered metabolism can be increased metabolism, decreased metabolism or a shift in the metabolic ratio of enantiomeric forms of a pharmaceutical drug in a mixture of enantiomers. The rate of altered pharmaceutical drugs metabolism due to polymorphic variants of CYP2D6 has been estimated at 7% of Caucasian Americans, 2% of African American and 1% of Asian Americans. However, the true rate of altered pharmaceutical drugs metabolism due to polymorphic variants of CYP2D6 and the distribution of CYP2D6 variants remains poorly understood, especially in individuals of non-northern European descent. Further, there remains large numbers of CYP2D6 variants that are, as yet, uncharacterized.

Due to time and cost limitations, phenotypic drug response variation due to the presence of

CYP2D6 variants is not adequately characterized during clinical trials of pharmaceutical drugs, but is only fully characterized once the pharmaceutical drug is used by the general population. There is currently no adequate method of screening a population prior to administration of pharmaceutical drugs in the general population to identify CYP2D6 variants in the population predictive of phenotypes likely to result in adverse reactions.

Therefore, there is a need for a method of screening a population to identify CYP2D6 variants in the population. Further, there is a need for a method of predicting adverse reactions to a pharmaceutical drug that is metabolized by the Cytochrome p450 isoenzyme CYP2D6. Additionally, there is a need to identify all variants of the Cytochrome p450 isoenzyme CYP2D6 that cause altered pharmaceutical drugs metabolism.

SUMMARY

In one embodiment of the present invention, there is provided a primer set that can be used to screen a polynucleotide sample to detect and identify variants in the Cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. The primer set comprises one or more than one primer group of the three primer groups of sequences selected from the primer groups consisting of Primer Group I (16 or more than 16 consecutive nucleotides of SEQ ID NO:9, 16 or more than 16 consecutive nucleotides of SEQ ID NO:10, 16 or more than 16 consecutive nucleotides of SEQ ID NO:11, 16 or more than 16 consecutive nucleotides of SEQ ID NO:12, 16 or more than 16 consecutive nucleotides of SEQ ID NO:13 and 16 or more than 16 consecutive nucleotides of SEQ ID NO:14); Primer Group II (16 or more than 16 consecutive nucleotides of SEQ ID NO:15, 16 or more than 16 consecutive nucleotides of SEQ ID NO:16; 16 or more than 16 consecutive nucleotides of SEQ ID NO:17, 16 or more than 16 consecutive nucleotides of SEQ ID NO:18, 16 or more than 16 consecutive nucleotides of SEQ ID NO:19, 16 or more than 16 consecutive nucleotides of SEQ ID NO:20, 16 or more than 16 consecutive nucleotides of SEQ ID NO:21, 16 or more than 16 consecutive nucleotides of SEQ ID NO:22, 16 or more than 16 consecutive nucleotides of SEQ ID NO:23 and 16 or more than 16 consecutive nucleotides of SEQ ID NO:24); and Primer Group III (16 or more than 16 consecutive nucleotides of SEQ ID NO:25; 16 or more than 16 consecutive nucleotides of SEQ ID NO:26; 16 or more than 16 consecutive nucleotides of SEQ ID NO:27, 16 or more than 16 consecutive nucleotides of SEQ ID NO:28, 16 or more than 16 consecutive nucleotides of SEQ ID NO:29, 16 or more than 16 consecutive

nucleotides of SEQ ID NO:30, 16 or more than 16 consecutive nucleotides of SEQ ID NO:31, and 16 or more than 16 consecutive nucleotides of SEQ ID NO:32).

In one embodiment, the primer set comprises two primer groups selected from the group consisting of Primer Group I, Primer Group II and Primer Group III. In another embodiment, the primer set comprises all three primer groups Primer Group I, Primer Group II and Primer Group III. In one embodiment, each sequence consists of at least 17 consecutive nucleotides. In another embodiment, each sequence consists of at least 18 consecutive nucleotides. In another embodiment, each sequence consists of at least 19 consecutive nucleotides. In another embodiment, each sequence consists of at least 20 consecutive nucleotides. In another embodiment, each sequence consists of at least 21 consecutive nucleotides. In another embodiment, one or more than one sequence additionally comprises a tail sequence. In another embodiment, one or more than one sequence has one or more than one dUTP substituted for TTP.

In another embodiment of the present invention, there is provided a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the sample. The method comprises a) providing a polynucleotide sample potentially comprising a sequence comprising at least about 50 consecutive nucleotides from one or more than one of the sequences of the wild type CYP2D6*1, SEQ ID NO:1, one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1 or both wild type CYP2D6*1, SEQ ID NO:1 and one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1; b) providing a primer set according to the present invention; c) amplifying the polynucleotide sample using the provided primer set to produce a set of amplicons; and d) analyzing the amplicons to identify the presence of CYP2D6*1 gene, SEQ ID NO:1, the presence of one or more than one variant of the CYP2D6*1 gene, SEQ ID NO:1 or to identify one or more than one specific variant of the CYP2D6*1 gene, SEQ ID NO:1 in the sample.

In another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second control individual, where the substance is metabolized by the CYP2D6 isoenzyme, and where the second control individual is homozygous for the wild type allele of the CYP2D6*1, SEQ ID NO:1. The method comprises a) providing a polynucleotide sample from the first individual; b) providing a primer set according to the present

invention; c) amplifying the polynucleotide sample using the provided primer set to produce a set of amplicons; d) analyzing the amplicons to detect and identify one or more than one variant in the CYP2D6 gene from the first individual; and e) analyzing the one or more than one variant in the CYP2D6 gene detected and identified to determine if it constitutes a silent variant or non-silent variant; where the absence of a non-silent variant means that the first individual will not have the potential for altered metabolism of the substance, and where the presence of a non-silent variant means that the first individual will have the potential for altered metabolism of the substance.

In another embodiment of the present invention, there is provided a method of screening a population to detect and identify the presence of one or more than one variant in the CYP2D6 gene. The method comprises a) providing a plurality of polynucleotide samples from the population; b) providing a primer set according to the present invention; c) amplifying the polynucleotide sample using the provided primer set to produce a set of amplicons; and d) analyzing the amplicons to detect and identify of one or more than one variant of the CYP2D6*1 gene, SEQ ID NO:1 in the sample. In one embodiment, the plurality of polynucleotide samples is a plurality of random samples of individuals in the population. In another embodiment, the plurality of polynucleotide samples is one or more than one sample from each individual in the population. In another embodiment, the method of screening a population further comprises determining the distribution of the variants in the CYP2D6 gene in the population. In another embodiment, the method of screening a population further comprises recording the presence and identity, or recording the distribution of the variants in the CYP2D6 gene in the population sample, in writing or another suitable media.

In a preferred embodiment, amplifying the polynucleotide sample in a method of the present invention comprises using modified nucleotides. In a particularly preferred embodiment, the modified nucleotides are selected from the group consisting of deaza dATP, deaza dGTP, and nucleotides labeled with one or more than one label selected from the group consisting of biotin, digoxigenin, and a fluorescent dye.

In a preferred embodiment, amplifying the polynucleotide sample in a method of the present invention comprises using dUTP in place of TTP. In another preferred embodiment, the amplification step in a method of the present invention is performed in two stages. In another preferred embodiment, analyzing the amplicons in a method of the present invention is performed

using a method selected from the group consisting of dideoxy sequencing, pyrosequencing and SSCP.

In another embodiment of the present invention, there is provided a kit for screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the sample, comprising suitable amounts of a primer set according to the present invention. In one embodiment, the kit further comprises one or more than one additional reagent or one or more than one vessel to amplify the polynucleotide sample, to analyze the amplicons, or both to amplify the polynucleotide sample and to analyze the amplicons. In a preferred embodiment, the additional reagent is selected from the group consisting of one or more than one DNA dependent polymerase, one or more than one buffer, one or more than one detergents and one or more than one stabilizing agent.

In another embodiment of the present invention, there is provided a purified or isolated variant of SEQ ID NO:1 having one or more than one of the alterations selected from the group consisting of C>T at position 1522, G insert at position 1576, G>C at position 1851, A>C at position 1852, A>G at position 1864, T>A at position 3230, C>T at position 3232, G>A at position 3335, C>T at position 3542, T>C at position 3617, A>G at position 3716, C>T at position 3922, G>T at position 4221, G>A at position 4280, G>A at position 4282, T>A at position 4379, T>C at position 4555, G>A at position 4607, C>T at position 4820, A>G at position 4854, T>C at position 4873, insert GT at position 4878, C>A at position 5003, T>C at position 5027, C>A at position 5054, C>T at position 5409, G>A at position 5496, C>T at position 5774, C>T at position 5791, C>T at position 5948, C>T at position 6020 and an exon 9 gene conversion.

In another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second control individual, where the substance is metabolized by the CYP2D6 isoenzyme, and where the second control individual is homozygous for the wild type allele of the CYP2D6*1, SEQ ID NO:1. The method comprises a) detecting and identifying one or more than one variant in the CYP2D6 gene from the first individual; and b) analyzing the one or more than one variant in the CYP2D6 gene detected and identified to determine if it constitutes one or more than one variant according to the present invention; where

the presence of the one or more than one variant means that the first individual will have the potential for altered metabolism of the substance.

In another embodiment of the present invention, there is provided a purified or isolated variant of SEQ ID NO:3 having one or more than one of the alterations selected from the group consisting of F>I at position 120, F>F at position 120, E>K at position 155, R>R at position 194, F>F at position 219, L>L at position 276, H>H at position 324, R>STOP at position 344, Y>C at position 355, H>H at position 361, V>FRAMESHIFT at position 363, E>K at position 418, H>Y at position 478, F>F at position 483.

In another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second control individual, where the substance is metabolized by the CYP2D6 isoenzyme, and where the second control individual is homozygous for the wild type allele of the CYP2D6*1, SEQ ID NO:1. The method comprises a) detecting and identifying one or more than one variant in the CYP2D6 isoenzyme from the first individual; and b) analyzing the one or more than one variant in the CYP2D6 isoenzyme detected and identified to determine if it constitutes one or more than one variant according to the present invention; where the presence of the one or more than one variant means that the first individual will have the potential for altered metabolism of the substance.

DESCRIPTION

According to one embodiment of the present invention, there is provided a primer set that can be used to screen a polynucleotide sample to detect and identify variants in the Cytochrome P450 isoenzyme 2D6 (CYP2D6) gene. According to another embodiment of the present invention, there is provided a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the sample. According to another embodiment of the present invention, there is provided a method of screening a population to detect and identify the presence of one or more than one variant in the CYP2D6 gene. According to another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second individual, where the substance is metabolized by the CYP2D6 isoenzyme. According to another embodiment of the present

invention, there is provided a kit for performing a method of the present invention. According to another embodiment of the present invention, there are provided novel purified and isolated variants of the Cytochrome p450 CYP2D6 gene and the CYP2D6 isoenzyme, including both silent variants and non-silent variants.

As used in this disclosure, the term "non-silent variant" refers to a CYP2D6 gene variant that causes a change in the production, regulation, length or sequence of the wild type CYP2D6 isoenzyme. As used in this disclosure, the term "silent variant" refers to a CYP2D6 gene variant that causes a change in the production, regulation, length or sequence of the wild type CYP2D6 isoenzyme. Both a non-silent variant and a silent variant can be the result of one or more than one point mutation that is a single nucleotide polymorphism, a deletion of one or more than one nucleotide, an insertion of one or more than one nucleotide, a gene conversion, or a combination of the preceding.

As used in this disclosure, the term "comprise" and variations of the term, such as "comprising" and "comprises," are not intended to exclude other additives, components, integers or steps.

The wild type allele of the CYP2D6 gene is designated as CYP2D6*1, GenBank accession number M33388, SEQ ID NO:1, and contains 9432 base pairs. The CYP2D6 gene is located on chromosome 22q13.1. The CYP2D6*1 gene, SEQ ID NO:1, is transcribed into an mRNA, GenBank accession number NM-000106, SEQ ID NO:2, that contains 9 exons, residues 1532-1799 of SEQ ID NO:1 (exon 1); residues 2503-2674 of SEQ ID NO:1 (exon 2); residues 3225-3377 of SEQ ID NO:1 (exon 3); residues 3466-3626 of SEQ ID NO:1 (exon 4); residues 4060-4236 of SEQ ID NO:1 (exon 5); residues 4427-4568 of SEQ ID NO:1 (exon 6); residues 4776-4963 of SEQ ID NO:1 (exon 7); residues 5418-5559 of SEQ ID NO:1 (exon 8); and residues 5658-5909 of SEQ ID NO:1 (exon 9). The CYP2D6 mRNA, SEQ ID NO:2, is translated into the wild type CYP2D6 isoenzyme, GenBank accession number AAA53500, SEQ ID NO:3, containing 497 amino acids.

There are a number of pseudogenes in the human genome on chromosome 22q close to the location of functional CYP2D6*1 gene, SEQ ID NO:1. These pseudogenes include GenBank accession number M33387, SEQ ID NO:4; GenBank accession number X58467, SEQ ID NO:5; GenBank accession number X58468, SEQ ID NO:6; GenBank accession number NG-000853,

SEQ ID NO:7; and GenBank accession number NG-000854; SEQ ID NO:8. These pseudogenes can cause false positive results in tests for variants of the CYP2D6 gene.

In one embodiment, the present invention is a primer set that can be used to interrogate a polynucleotide sample to detect and identify variants in the Cytochrome P450 isoenzyme 2D6 (CYP2D6) gene, and thereby, to detect and identify variants in the Cytochrome P450 2D6 (CYP2D6) isoenzyme. The variants include differences in the sequence of the CYP2D6 gene that can affect the function of the translated CYP2D6 isoenzyme by changing the production, regulation, length or sequence of the CYP2D6 isoenzyme compared to the wild type CYP2D6 isoenzyme, and differences in the sequence of the CYP2D6 gene that code for 5' and 3' untranslated regions and for flanking intronic sequences that effect the production, regulation, length or sequence of the transcribed messenger RNA, and combinations of the preceding. The primer set permits amplification from a small polynucleotide sample of selected portions of the coding portion of the CYP2D6 gene, or amplification of the entire coding portion of the CYP2D6 gene, as well as the flanking intronic sequences that are relevant to recognition of splice sites. The primer set further permits the detection of genetic variants of the CYP2D6 gene without interference from pseudogenes, or from homologous or paralogous genes of non-CYP2D6 Cytochrome p450 genes. The primer set also permits the detection of low frequency variants that affect pharmaceutical drugs metabolism, thereby decreasing the false negative rate in variant screening.

TABLE I

EXAMPLES OF PRIMERS

SEQ ID NO:	AMPLIFICATION REGION	AMPLIFICATION DIRECTION	SEQUENCE	AMPLICON SIZE	GROUP
9	EXON 1-2	FORWARD	5'AGCAGAGGGCAAAGGCCATCA	1281	I
10	EXON 1-2	REVERSE	5'CTCTCTGCCCAGCTCGGACTA	1281	I
11	EXON 1	FORWARD	5'CTTTATAAGGGAAGGGTCACG	346	I
12	EXON 1	REVERSE	5'AGGGGAGCCTCAGCACCTCTG	346	I
13	EXON 2	FORWARD	5'GGTGATCCTGGCTTGACAAGA	251	I
14	EXON 2	REVERSE	5'CCACGGAAATCTGTCTCTGTC	251	I
15	EXON 3-6	FORWARD	5'TGGTGGGGCTAATGCCTTCAT	1559	II
16	EXON 3-6	REVERSE	5'CCGGCCCCTGACACTCCTTCT	1559	II
17	EXON 3	FORWARD	5'GGTGGATGGTGGGGCTAATGC	252	II
18	EXON 3	REVERSE	5'CTTCCCAGTTCCCGCTTTGTG	252	II
19	EXON 4	FORWARD	5'ACGGGGAAGGCGACCCCTTAC	242	II
20	EXON 4	REVERSE	5'GAGCTCGCCCTGCAGAGACTC	242	II
21	EXON 5	FORWARD	5'AGAGCACAGGAGGGATTGAGA	277	II
22	EXON 5	REVERSE	5'ATTCCTCCTGGGACGCTCAAC	277	II
23	EXON 6	FORWARD	5'CCGTTCTGTCCCGAGTATGCT	207	II
24	EXON 6	REVERSE	5'CCCCTGCACTGTTTCCCAGAT	207	II
25	EXON 7-9	FORWARD	5'GGAGGCAAGAAGGAGTGTCAG	1397	III
26	EXON 7-9	REVERSE	5'ACCAATCTGGGCAGTCAGAGT	1397	III
27	EXON 7	FORWARD	5'GGCCGGACCCCCTGGGTGCTG	277	III
28	EXON 7	REVERSE	5'GCTGGTGCTGAGCTGGGGTGA	277	III
29	EXON 8	FORWARD	5'TAGAGTCCAGTCCCCACTCTC	227	III
30	EXON 8	REVERSE	5'AGACTCCACGGAAGGGGACAG	227	III
31	EXON 9	FORWARD	5'TCACCCAGGAGCCAGGCTCAC	332	III
32	EXON 9	REVERSE	5'TGATCCCAACGAGGGCGTGAG	332	III

The primer set of the present invention comprises a plurality of primers selected from the group consisting of the primers shown in Table I. In a preferred embodiment, the present invention comprises one or more than one primer group of the three primer groups selected from the primer groups consisting of Primer Group I (SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11,

SEQ ID NO:12, SEQ ID NO:13 and SEQ ID NO:14); Primer Group II (SEQ ID NO:15, SEQ ID NO:16; SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 and SEQ ID NO:24); and Primer Group III (SEQ ID NO:25; SEQ ID NO:26; SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31 and SEQ ID NO:32). In a preferred embodiment of the present invention, the primer set comprises two primer groups selected from the group consisting of Primer Group I, Primer Group II and Primer Group III. In a particularly preferred embodiment, the primer set comprises all three primer groups, Primer Group I, Primer Group II and Primer Group III.

Each primer, SEQ ID NO:9 through SEQ ID NO:32, is shown having exactly 21 nucleotides. However, as will be understood by those with skill in the art with reference to this disclosure, each primer can be truncated to contain less than 21 nucleotides. In one embodiment, one or more than one primer consists of only 16 consecutive nucleotides, only 17 consecutive nucleotides, only 18 consecutive nucleotides, only 19 consecutive nucleotides, or only 20 consecutive nucleotides of the sequences disclosed. Truncating the primer will usually decrease the binding efficiency of the primer and can cause less specific binding. Thus, in a preferred embodiment, the primer set comprises primers having the full sequences shown in Table I for maximum efficiency. However, truncated primers will usually still work in the methods of the present invention.

Additionally, primers from the primer set of the present invention can include added tail sequences, in particular at their 5' ends. Examples of suitable include -40 M13 Forward Promer, -21 M13 Forward Primer, -28 M13 Reverse Primer, -28 M13 Reverse 2 Primer, -29 M13 Reverse Primer, SP6 Primer, T7 Primer, T3 Primer, and Poly T (16-24 nucleotides) Primer. However, other tail sequences can also be used, as will be understood by those with skill in the art with reference to this disclosure. The addition of tail sequences is particularly preferred when the primers are truncated, in order to increase their binding efficiency as will be understood by those with skill in the art with reference to this disclosure. Further, dUTP can be substituted for TTP in a primer, as will be understood by those with skill in the art with reference to this disclosure.

Primer Group 1 is used to amplify the region of the CYP2D6 gene, SEQ ID NO:1, containing residues 1532-1799 of SEQ ID NO:1 (exon 1); and residues 2503-2674 of SEQ ID NO:1 (exon 2). Primer Group II is used to amplify the region of the CYP2D6 gene, SEQ ID

NO:1, containing residues 3225-3377 of SEQ ID NO:1 (exon 3); residues 3466-3626 of SEQ ID NO:1 (exon 4); residues 4060-4236 of SEQ ID NO:1 (exon 5); and residues 4427-4568 of SEQ ID NO:1 (exon 6). Primer Group III is used to amplify the region of the CYP2D6 gene, SEQ ID NO:1, containing residues 4776-4963 of SEQ ID NO:1 (exon 7); residues 5418-5559 of SEQ ID NO:1 (exon 8); and residues 5658-5909 of SEQ ID NO:1 (exon 9).

In another embodiment, the present invention is a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the sample. The method comprises, first, providing a polynucleotide sample potentially comprising a sequence comprising at least about 50 consecutive nucleotides from one or more than one of the sequences of the wild type CYP2D6*1, SEQ ID NO:1, one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1 or both wild type CYP2D6*1, SEQ ID NO:1 and one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1. The polynucleotide sample can originate from a human, a nonhuman animal including a transgenic animal or clone, or from another suitable source, as will be understood by those with skill in the art with reference to this disclosure. The polynucleotide sample can be in the form of one or more than one peripheral whole blood sample, buccal swab, Guthrie blood spot, preserved tissues sample such as a liver sample, paraffin embedded tissue, or from a clone library, or from another suitable source, as will be understood by those with skill in the art with reference to this disclosure.

Next, the method comprises providing a primer set according to the present invention. Then, the method comprises amplifying the polynucleotide sample using the provided primer set. Amplification can be performed using standard PCR, using the method as disclosed in United States Patent 6,322,988 to Dawson et al, the contents of which are incorporated into this disclosure by reference in their entirety, or using another amplification method as will be understood by those with skill in the art with reference to this disclosure.

Additionally, as will be understood by those with skill in the art with reference to this disclosure, modified nucleotides, such as deaza dATP or deaza dGTP, can be used in the amplification step in conjunction with high denaturation temperatures, or for other reasons such as when the sequence of the CYP2D6 gene to be amplified contains high G/C or high A/T, and dUTP can be substituted for TTP. Further, modified bases in the form of their deoxynucleotide triphosphate can be used in the amplification step to introduce labels, such as biotin, digoxigenin

or fluorescent dyes, such as fluoresceine, to produce labeled amplification products. The labeled amplification products can then be identified using array technology or can be used for other purposes, as will be understood by those with skill in the art with reference to this disclosure.

In a preferred embodiment, the amplification step is performed in two stages. The amplification step can be used to amplify a region of the CYP2D6 gene containing 1532-1799 of SEQ ID NO:1 (exon 1) and residues 2503-2674 of SEQ ID NO:1 (exon 2) using Primer Group I; or containing residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5) and residues 4427-4568 of SEQ ID NO:1 (exon 6) using Primer Group II; or containing residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9) using Primer Group III; or containing 1532-1799 of SEQ ID NO:1 (exon 1), residues 2503-2674 of SEQ ID NO:1 (exon 2), residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5) and residues 4427-4568 of SEQ ID NO:1 (exon 6) using Primer Group I and Primer Group II; or containing 1532-1799 of SEQ ID NO:1 (exon 1), residues 2503-2674 of SEQ ID NO:1 (exon 2), residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9) using Primer Group I and Primer Group III; or containing residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5), residues 4427-4568 of SEQ ID NO:1 (exon 6), residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9) using Primer Group II and Primer Group III; or containing 1532-1799 of SEQ ID NO:1 (exon 1), residues 2503-2674 of SEQ ID NO:1 (exon 2), residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5), residues 4427-4568 of SEQ ID NO:1 (exon 6), residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9) using Primer Group I, Primer Group II and Primer Group III. In a preferred embodiment, the amplification step is used to amplify a region of the CYP2D6 gene containing 1532-1799 of SEQ ID NO:1 (exon 1), residues 2503-2674 of SEQ ID NO:1 (exon 2), residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5), residues 4427-4568 of SEQ ID NO:1 (exon 6),

residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9) using Primer Group I, Primer Group II and Primer Group III.

Though the amplification step will now be disclosed in the context of using all three primer groups, Primer Group I, Primer Group II and Primer Group III, to amplify regions of the CYP2D6 gene containing 1532-1799 of SEQ ID NO:1 (exon 1), residues 2503-2674 of SEQ ID NO:1 (exon 2), residues 3225-3377 of SEQ ID NO:1 (exon 3), residues 3466-3626 of SEQ ID NO:1 (exon 4), residues 4060-4236 of SEQ ID NO:1 (exon 5), residues 4427-4568 of SEQ ID NO:1 (exon 6), residues 4776-4963 of SEQ ID NO:1 (exon 7), residues 5418-5559 of SEQ ID NO:1 (exon 8) and residues 5658-5909 of SEQ ID NO:1 (exon 9), amplifying shorter regions of the CYP2D6 gene can be performed with corresponding procedures using either one primer group or two primer groups, as will be understood by those with skill in the art with reference to this disclosure.

In the first amplification stage, three regions of the CYP2D6 gene are amplified using the six primers, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:25 and SEQ ID NO:26. The first amplification stage can be performed, for example, using standard PCR as follows, though other methods can also be used as will be understood by those with skill in the art with reference to this disclosure. By way of example only, first, a sample of 1 μl of 1xT.E. buffer containing 20 ng of a polynucleotide sample is provided potentially comprising at least 50 consecutive nucleotides from one or more than one sequence selected from the group consisting of the wild type CYP2D6*1, SEQ ID NO:1, one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1 and both the wild type CYP2D6*1, SEQ ID NO:1 and one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1. Then, 19 μl of buffer is added to the polynucleotide sample. The 19 μl of buffer contains 0.2-2.0 units of Taq Gold, 200 μM each of dATP, dCTP, dGTP and TTP, 2 mM $MgCl_2$, 50 mM KCl, 5 mM dithiothreitol 2% DMSO, 10 mM TRIS/TRIS HCl, pH 9.0, and 10 pMoles of one primer pair selected from the group consisting of SEQ ID NO:9 and SEQ ID NO:10; SEQ ID NO:15 and SEQ ID NO:16; and SEQ ID NO:25 and SEQ ID NO:26. The buffered polynucleotide sample is then thermocycled using a standard thermocycler and standard vessels, and using a first cycle of 95°C for 12 minutes to activate the Taq Gold, followed by 30-40 cycles consisting of denaturation at 95°C for 30

seconds, annealing at 62°C for 30 seconds, extension at 72°C for 2 minutes, and a final extension at 72°C for 8 minutes. Then, the amplification is repeated twice more on the same sample using each additional primer pair of the three primer pairs until the sample has been amplified using all three primer pairs. In a preferred embodiment, the first amplification stage is performed using two of the three primer pairs simultaneously, rather than sequentially, following by an amplification using the third primer pair. In a particularly preferred embodiment, the amplification is performed using all three primer pairs simultaneously. Performing the amplification using each of the three primer pairs sequentially rather than simultaneously is particularly preferred if the analysis method to be used to sequence the amplicons disclosed below, such as SSCP, would function less optimally on the amplicons produced by all three primer pairs simultaneously, as will be understood by those with skill in the art with reference to this disclosure. This first amplification stage results in a sample comprising three amplicons containing 1532-1799 of SEQ ID NO:1 exons 1-2; exons 3-6; and exons 7-9, as well as the four flanking intronic sequences that effect the production, regulation, length or sequence of the transcribed messenger RNA (or in a sample comprising one or two of these amplicons and flaking intronic sequences, if less than all three primer pairs are used in the first amplification stage, as will be understood by those with skill in the art with reference to this disclosure).

Next, the sample comprising the amplicons resulting from the first amplification stage is subjected to a second amplification stage using some or all of the 18 remaining primers from the primer set of the present invention; SEQ ID NO:11 through SEQ ID NO:14, SEQ ID NO:17 through SEQ ID NO:24, and SEQ ID NO:27 through SEQ ID NO:32. First, 1 μl of sample resulting from the first amplification stage is diluted 1:1000 in 0.1xT.E. buffer. Then, 19 μl of buffer is added to the diluted sample. The 19 μl of buffer contains 0.2-2.0 units of Taq Gold, 200 μM each of dATP, dCTP, dGTP and TTP, 2 mM $MgCl_2$, 50 mM KCl, 5 mM dithiothreitol 2% DMSO, 10 mM TRIS/TRIS HCl, pH 9.0, and 10 pMoles each of one or more than one primer pair, depending on the exon or exons of interest as follows: SEQ ID NO:11 and SEQ ID NO:12 for 1532-1799 of SEQ ID NO:1 (exon 1); SEQ ID NO:13 and SEQ ID NO:14 for residues 2503-2674 of SEQ ID NO:1 (exon 2); SEQ ID NO:17 and SEQ ID NO:18 for residues 3225-3377 of SEQ ID NO:1 (exon 3); SEQ ID NO:19 and SEQ ID NO:20 for residues 3466-3626 of SEQ ID NO:1 (exon 4); SEQ ID NO:21 and SEQ ID NO:22 for residues 4060-4236 of SEQ ID NO:1

(exon 5); SEQ ID NO:23 and SEQ ID NO:24 for residues 4427-4568 of SEQ ID NO:1 (exon 6); SEQ ID NO:27 and SEQ ID NO:28 for residues 4776-4963 of SEQ ID NO:1 (exon 7); SEQ ID NO:29 and SEQ ID NO:30 for residues 5418-5559 of SEQ ID NO:1 (exon 8); or SEQ ID NO:31 and SEQ ID NO:32 for residues 5658-5909 of SEQ ID NO:1 (exon 9), as will be understood by those with skill in the art with reference to this disclosure. The sample is then thermocycled using a standard thermocycler and standard vessels, and using a first cycle of 95°C for 12 minutes to activate the Taq Gold, followed by 30-40 cycles consisting of denaturation at 95°C for 30 seconds, annealing at 62°C for 30 seconds, extension at 72°C for 2 minutes, and a final extension at 72°C for 8 minutes. Then, the one or more than one primer pair used depends on the amplicons in the sample that resulted from the first amplification stage. If, for example, all three primer pairs, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:25 and SEQ ID NO:26, were used in the first amplification stage, and the amplicons of interest include all 9 exons, then all remaining nine primer pairs are used in the second amplification stage. If only one or only two primer pairs were used in the first amplification stage, then fewer than all nine remaining primer pairs can be used in the second amplification stage, as will be understood by those with skill in the art with reference to this disclosure. In a preferred embodiment, the second amplification stage is performed using all nine primer pairs, SEQ ID NO:11 through SEQ ID NO:14, SEQ ID NO:17 through SEQ ID NO:24, and SEQ ID NO:27 through SEQ ID NO:32, simultaneously. In another preferred embodiment, the second amplification stage is performed using all nine primer pairs but where one or more than one of the nine primer pairs are used sequentially rather than simultaneously. When all nine primer pairs are used in the second amplification stage after a first amplification stage involving three primer pairs, the second amplification results in nine amplicons, each amplicon containing one exon as well as the four flanking intronic sequences that affect the production, regulation, length or sequence of the transcribed messenger RNA (or in fewer than nine amplicons and flaking intronic sequences if less than all eighteen primer pairs are used in the second amplification stage, as will be understood by those with skill in the art with reference to this disclosure).

The amplicons produced using the present method represent polynucleotides distinct from CYP2D6 pseudogenes, and from homologous or paralogous genes related to the CYP2D6 gene, thereby eliminating these sources of potential false positive results of the presence of variants.

Further, since the present method amplifies only exons and their adjacent flanking intronic sequences, the method produces amplicons that are relevant to identifying only variants of the CYP2D6 gene having an effect of the CYP2D6 isoenzyme, SEQ ID NO:3.

Next, the method comprises analyzing the amplicons produced in the second amplification stage to identify the presence of CYP2D6*1 gene, SEQ ID NO:1, the presence of a variant of the CYP2D6*1 gene, SEQ ID NO:1 or to identify the specific variant of the CYP2D6*1 gene, SEQ ID NO:1 in the sample. This analysis step can be performed using any suitable method, such as dideoxy sequencing, pyrosequencing, SSCP or another suitable method, as will be understood by those with skill in the art with reference to this disclosure.

According to another embodiment of the present invention, there is provided a method of screening a population to detect and identify the presence of one or more than one variant in the CYP2D6 gene. The method comprises providing a plurality of polynucleotide samples from the population, where the plurality of polynucleotide samples is selected from a representative group of individuals from the population, such as for example, a plurality of random samples of individuals in the population or one or more than one sample from each individual in the population. Next, each of the pluralities of polynucleotide samples is subjected to a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the polynucleotide sample according to the present invention. In a preferred embodiment, the method further comprises determining the distribution of the variants in the CYP2D6 gene in the population. In another preferred embodiment, the method comprises recording the presence and identity, or recording the distribution of the variants in the CYP2D6 gene in the population sample, in writing or another suitable media.

According to another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second control individual, where the substance is metabolized by the CYP2D6 isoenzyme, and where the second control individual is homozygous for the wild type allele of the CYP2D6*1, SEQ ID NO:1. In one embodiment, the method comprises, first, providing a polynucleotide sample from the first individual. Next, the polynucleotide sample from the first individual is subjected to a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the

CYP2D6 gene in the polynucleotide sample according to the present invention. Then, the one or more than one variant in the CYP2D6 gene detected and identified is analyzed to determine if it constitutes a silent variant or non-silent variant, where the absence of a non-silent variant means that the first individual will not have the potential for altered metabolism of the substance, and where the presence of a non-silent variant means that the first individual will have the potential for altered metabolism of the substance.

According to another embodiment of the present invention, there are provided novel purified and isolated variants of the Cytochrome p450 CYP2D6 gene and corresponding variants in the CYP2D6 isoenzyme, including both silent variants and non-silent variants. The variants were detected and identified using the methods of the present invention. The variants are disclosed in Table II. Further, some individuals had a plurality of the variants listed in Table I. The present invention, therefore, includes both the 32 variants of the Cytochrome p450 CYP2D6 gene and corresponding variants in the CYP2D6 isoenzyme, if any, as well as variants of the Cytochrome p450 CYP2D6 gene having a plurality of the variants listed in Table I, and corresponding variants in the CYP2D6 isoenzyme, if any.

TABLE II

VARIANTS OF THE CYTOCHROME P450 CYP2D6 GENE AND CORRESPONDING VARIANTS IN THE CYP2D6 ISOENZYME

VARIANT NUMBER	POSITION CHANGE IN WILD TYPE SEQUENCE, SEQ ID NO:1	POSITION CHANGE IN WILD TYPE SEQUENCE, SEQ ID NO:1, NUMBERED FROM ATG (MET)	VARIANT	POSITION CHANGE IN WILD TYPE POLYPEPTIDE SEQUENCE, SEQ ID NO:3	VARIANT
1	1522	-98	C>T		
2	1576	-44	insert GUIDING TUBE		
3	1851	232	G>C		
4	1852	233	A>C		
5	1864	245	A>G		
6	3230	1611	T>A	120	F>I
7	3232	1613	C>T	120	F>F
8	3335	1716	G>A	155	E>K
9	3542	1923	C>T	194	R>R
10	3617	1998	T>C	219	F>F
11	3716	2097	A>G		
12	3922	2303	C>T		
13	4221	2602	G>T	276	L>L
14	4280	2661	G>A		
15	4282	2663	G>A		
16	4379	2760	T>A		
17	4555	2936	T>C	324	H>H
18	4607	2988	G>A		
19	4820	3201	C>T	344	R>STOP
20	4854	3235	A>G	355	Y>C
21	4873	3254	T>C	361	H>H
22	4878	3259	insert GT	363	V>FRAME SHIFT
23	5003	3384	C>A		
24	5027	3408	T>C		
25	5054	3435	C>A		
26	5409	3790	C>T		
27	5496	3877	G>A	418	E>K
28	5774	4155	C>T	478	H>Y
29	5791	4172	C>T	483	F>F
30	5948	4329	C>T		
31	6020	4401	C>T		

32	EXON9		GENE CONVERSION	

According to another embodiment of the present invention, there is provided a method of predicting the potential for altered metabolism of a substance, including one or more than one pharmaceutical drug, by a first individual compared to a second control individual, where the substance is metabolized by the CYP2D6 isoenzyme, and where the second control individual is homozygous for the wild type allele of the CYP2D6*1, SEQ ID NO:1. In one embodiment, the method comprises, first, providing a polynucleotide sample from the first individual. Next, the polynucleotide sample from the first individual is subjected to a method of screening a polynucleotide sample to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the polynucleotide sample according to the present invention. Then, the one or more than one variant in the CYP2D6 gene detected and identified is analyzed to determine if it constitutes one of the novel non-silent variants of the present invention, where the presence of one of the novel non-silent variants of the present invention means that the first individual will have the potential for altered metabolism of the substance.

In another embodiment, the present invention is a kit for performing a method of the present invention. The kit comprises suitable amounts of one or more than one primer group selected from the group consisting of Primer Group I, Primer Group II and Primer Group III to perform the amplification step of a method of the present invention. In one embodiment, the kit comprises suitable amounts of two primer groups selected from the group consisting of Primer Group I and Primer Group II; and Primer Group I and Primer Group III; and Primer Group II and Primer Group III. In a preferred embodiment, the kit comprises suitable amounts of all three primer groups Primer Group I, Primer Group II and Primer Group III. Additionally, the kit can comprise additional reagents or vessels for performing a method of the present invention, such as one or more than one DNA dependent polymerase, one or more than one buffer, one or more than one detergents and one or more than one stabilizing agent. Further, the kit can comprise reagents or vessels for analyzing or sequencing the amplicons resulting from a method of the present invention. Additionally, the kit can comprise written or recorded directions for performing a method of the present invention.

EXAMPLE

METHOD OF SCREENING A POLYNUCLEOTIDE SAMPLE TO DETECT AND IDENTIFY THE PRESENCE OF ONE OR MORE THAN ONE VARIANT IN THE CYP2D6 GENE IN THE SAMPLE

A polynucleotide sample was screened to detect and identify the presence of one or more than one variant in the CYP2D6 gene in the sample according to the present invention as follows. First, polynucleotide samples were provided that potentially comprises a sequence comprising at least about 50 consecutive nucleotides from one or more than one of the sequences of the wild type CYP2D6*1, SEQ ID NO:1, one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1 or both wild type CYP2D6*1, SEQ ID NO:1 and one or more than one variant of wild type CYP2D6*1, SEQ ID NO:1. The polynucleotide samples provided were human diversity panels of genomic DNA obtained from Corriel Laboratories. The panels consisted of 10 μg of genomic DNA each from a first group of 100 African Americans, a second group of 10 African Americans, 100 Caucasians, 10 Chinese Asians, 10 Japanese Asians, 10 non-Chinese, non-Japanese Asians, and 20 aged controls. Next, the samples were dried in a SpeedVac™ (Thermo Savant, Inc., Holbrook, NY US) and then, resuspended in 1xT.E. buffer (1xT.E. = 1 mM EDTA, 10mM TrisHCl) having a pH 7.6 to a concentration of 200 ng/μl per sample. Stock samples were stored at -20°C until ready for dispensing.

Once the samples were ready for dispensing, the samples were thawed and allowed to come to room temperature. Then, the samples were further diluted with 0.1xT.E. to a concentration of 2 ng/μl. The samples were then dispensed in 10 μl increments to individual wells of 96 well 200 μl PCR plates. The plated samples were then dried in an oven at between 60°C and 70°C for one hour until no visible moisture was observed in the wells of the plates. The dried samples in plates were then stored with a desiccant at room temperature in sealed containers until ready for amplification.

Next, the samples were subjected to a two-stage amplification procedure according to the present invention, using PCR. First, 20 μl of a master mix was added to each well. The master mix consisted of an aqueous buffer of 0.25 units of TAQ Gold ™ (PE Applied Biosystems, Inc. Foster City, CA US), 2 mM $MgCl_2$, 50 mM KCl, 10mM TrisHCl, pH 9.0 and 10 pMoles of each primer of the six primers, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:15, SEQ ID NO:16, SEQ

ID NO:25 and SEQ ID NO:26 as appropriate for the specific region of the CYP2D6 gene being amplified. The first amplification stage was conducted on thermocyclers (MJ Research, Inc., Cambridge, MA US) using a set of cycles consisting of 95°C for 12 minutes, followed by a cycle consisting of denaturation at 95°C for 30 seconds, a cycle of annealing at 60°C for 20 seconds, and cycles of extension at 72°C for 1 minute and 40 seconds. These three steps of cycling were repeated 34 additional times followed by a final cycle of extension at 72°C for 8 minutes.

Then, 2 μl of the resulting amplicons were electrophoresed on 1% precast agarose gel containing ethidium bromide. The amplicons were stored at -20°C until the second amplification stage.

Next, the amplicons from the first amplification stage were subjected to a second amplification stage. First, the amplicons were treated with ExoSap® (USB Corporation, Cleveland, OH US) using 1 μl of the enzyme mixture added directly to the amplicons in the wells of the 96 well plate in which they were originally subjected to the first amplification stage, and the plated amplicons were heated for 1 hour at 37°C, followed by heat inactivation at 65°C for 30 minutes, followed by heating at 80°C for 10 minutes, and then followed by cooling to 4°C.

One group of the ExoSap® treated samples were amplified using components from a core cycle sequencing kit (PE Applied Biosystems, Inc., Foster City, CA US). The amplification reaction was performed on 20 μl of substrate comprising the 2 μl treated sample (containing about 100 ng of amplicons), 10 pMoles each of exon specific primer pairs according to the present invention, (SEQ ID NO:11 through SEQ ID NO:14, SEQ ID NO:17 through SEQ ID NO:24, and SEQ ID NO:27 through SEQ ID NO:32), 2 units of FS polymerase, 4 μl of 5x reaction buffer and 1 μl each of the A and C terminator mixes, with the balance consisting of 18 megaohm water. The amplification reactions were performed in the wells of a 96 well PCR plate or in 200 μl PCR strip tubes (Fisher Scientific L.L.C., Pittsburgh, PA US) using cycling conditions consisting of a first denaturation step of 95°C for 5 minutes, followed by 35 cycles of three steps consisting of heating at 95°C for 30 seconds, annealing at 55°C for 20 seconds, and extension at 60°C for 4 minutes, followed by cooling to 4°C. Reactions were then cleaned to remove unincorporated terminators using a microtiter cleanup system (Millipore Corporation, Bedford, MA US).

The recovered 20 μl filtrates were then dried in the wells of a fresh 96 well plate under vacuum at 60°C in a SpeedVac™ after the addition of 1 μl and a tetramethylrhodamine labeled

MapMarker® TMR 650 (BioVentures, Inc., Murfreesboro, TN US). The dried products were resuspended in 3 μl of 18 megaohm water and 3 μl of a mix of deionized formamide (American Bioanalytical Products, Natick, MA US). Next, the samples were denatured and concentrated to about 3 μl by heating at 95°C for 10 minutes without an evaporation barrier and then cooled to 4°C.

1.2 μl of the denatured and concentrated samples were loaded onto individual teeth of a 50 tooth gel loading comb (The Gel Company, San Francisco, CA US) and then loaded onto the gels of an ABI Prism 377 DNA Sequencer (PE Applied Biosystems, Inc. Foster City, CA US) using the comb manufacturer's suggested protocol. The terminated polynucleotide fragments were analyzed on 0.2 mm thick 36 cm denaturing Long Ranger® polyacrylamide gels (FMC Corporation, Philadelphia, PA US) prepared using the instrument manufacturer's and the gel manufacturer's instructions. The gels were prepared 18 hours prior to use to assure complete polymerization of the acrylamide. The run conditions utilized were those recommended by the instrument manufacturer for performing dye terminated sequencing reactions for the core kit.

Sequencing reactions were also performed using 1 μl of sample (comprising about 50 ng of amplicons) of the treated PCR products and components from a Big Dye sequencing kit (PE Applied Biosystems, Inc. Foster City, CA US) setting up separate forward and reverse sequencing reactions using the exon specific forward or reverse primers, (SEQ ID NO:11 through SEQ ID NO:14, SEQ ID NO:17 through SEQ ID NO:24, and SEQ ID NO:27 through SEQ ID NO:32), according to the present invention specific for the region being sequenced. Modifications were made to the manufacturer's suggested protocol consisting of reducing the primer concentrations to 2.4 pMoles per reaction and using 4 μl of the supplied Ready Reaction Mix™ for each 20 μl reaction. Cycle sequencing was performed in 96 well plates using the recommended thermocycling conditions on a thermocycler. The reaction components were then cleaned to remove unincorporated terminators using a microtiter cleanup system.

Following the sequencing reaction, the terminated products were obtained by precipitation using the manufacturer's suggested procedure. The dried fragments obtained by this procedure were resuspended in 3 μl of 18 megaohm water and 3 μl of formamide. Samples were denatured uncapped at 95°C for 10 minutes which reduced volume to about 3 μl. 1.2 μl of each sample was loaded onto the teeth of a 50-lane loading comb following manufacturer's protocol. Terminated

fragments were electrophoresed on an ABI Prism 377 DNA Sequencer using the manufacturer's recommended procedure using 0.2 mm thick Long Ranger® polyacrylamide gels.

The sequence data obtained from both sequencing procedures were analyzed using fragment analysis software and compared to sequence data for the wild type CYP2D6*1gene sequence, SEQ ID NO:1. The data obtained from the procedures revealed a plurality of variants of the CYP2D6 gene present in the samples that were not previously reported, especially in samples from Asians and African Americans.

Although the present invention has been discussed in considerable detail with reference to certain preferred embodiments, other embodiments are possible. Therefore, the scope of the appended claims should not be limited to the description of preferred embodiments contained in this disclosure.